

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Caras, Ingrid W

(ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 1 DNA Way

(C) CITY: South San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/635130

(B) FILING DATE: 19-Mar-1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Torchia, PhD., Timothy E.

(B) REGISTRATION NUMBER: 36,700

(C) REFERENCE/DOCKET NUMBER: P1001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-8674

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1877 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: Extra Cellular Domain

(B) LOCATION: 244-899

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: Transmembrane Domain
- (B) LOCATION: 901-978
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(ix) FEATURE:

- (A) NAME/KEY: signal peptide
- (B) LOCATION: 244-321
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GNTCTAGAAN TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCCT 50
GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
TTTGGGGGAG TTGGTGCCCC GCCCCCCAGG CCTTGCGGGG GTC ATG 246
Met
1
GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
5 10
GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
15 20 25
CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
30 35 40
AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402
Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
45 50
ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
55 60 65
CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480
Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr
70 75

AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519
 Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys
 80 85 90

GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558
 Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
 95 100 105

CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597
 Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln
 110 115

GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636
 Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser
 120 125 130

CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675
 His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr
 135 140

CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714
 Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu
 145 150 155

ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753
 Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser
 160 165 170

CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792
 Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu
 175 180

ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831
 Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu
 185 190 195

GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870
 Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser
 200 205

AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT 909
 Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro
 210 215 220

CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG 948
 Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu
 225 230 235

GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987
 Ala Leu Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala

240

245

ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT 1026
Met Cys Trp Arg Arg Arg Arg Ala Lys Pro Ser Glu Ser
250 255 260

CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT 1065
Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser
265 270

CTG GGC CTG GGG GGT GGA GGT GGG ATG GGA CCT CGG GAG 1104
Leu Gly Leu Gly Gly Gly Gly Gly Met Gly Pro Arg Glu
275 280 285

GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC 1143
Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly
290 295 300

GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG 1182
Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys
305 310

GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG 1221
Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln
315 320 325

GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA 1260
Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr
330 335

TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA 1299
Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile
340 345 350

CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT 1338
Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr
355 360 365

ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT 1377
Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr
370 375

TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA 1416
Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro
380 385 390

TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA 1455
Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg
395 400

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Tyr | Glu | Phe | Tyr | Lys | Leu | Tyr | Leu | Val | Gly | Gly | Ala | Gln | Gly | Arg | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Arg | Cys | Glu | Ala | Pro | Pro | Ala | Pro | Asn | Leu | Leu | Leu | Thr | Cys | Asp | |
| | | | | 95 | | | | | 100 | | | | | 105 | |
| Arg | Pro | Asp | Leu | Asp | Leu | Arg | Phe | Thr | Ile | Lys | Phe | Gln | Glu | Tyr | |
| | | | | 110 | | | | | 115 | | | | | 120 | |
| Ser | Pro | Asn | Leu | Trp | Gly | His | Glu | Phe | Arg | Ser | His | His | Asp | Tyr | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Tyr | Ile | Ile | Ala | Thr | Ser | Asp | Gly | Thr | Arg | Glu | Gly | Leu | Glu | Ser | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Leu | Gln | Gly | Gly | Val | Cys | Leu | Thr | Arg | Gly | Met | Lys | Val | Leu | Leu | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Arg | Val | Gly | Gln | Ser | Pro | Arg | Gly | Gly | Ala | Val | Pro | Arg | Lys | Pro | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Val | Ser | Glu | Met | Pro | Met | Glu | Arg | Asp | Arg | Gly | Ala | Ala | His | Ser | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Leu | Glu | Pro | Gly | Lys | Glu | Asn | Leu | Pro | Gly | Asp | Pro | Thr | Ser | Asn | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Ala | Thr | Ser | Arg | Gly | Ala | Glu | Gly | Pro | Leu | Pro | Pro | Pro | Ser | Met | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Pro | Ala | Val | Ala | Gly | Ala | Ala | Gly | Gly | Leu | Ala | Leu | Leu | Leu | Leu | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Gly | Val | Ala | Gly | Ala | Gly | Gly | Ala | Met | Cys | Trp | Arg | Arg | Arg | Arg | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ala | Lys | Pro | Ser | Glu | Ser | Arg | His | Pro | Gly | Pro | Gly | Ser | Phe | Gly | |
| | | | | 260 | | | | | 265 | | | | | 270 | |
| Arg | Gly | Gly | Ser | Leu | Gly | Leu | Gly | Gly | Gly | Gly | Gly | Met | Gly | Pro | |
| | | | | 275 | | | | | 280 | | | | | 285 | |
| Arg | Glu | Ala | Glu | Pro | Gly | Glu | Leu | Gly | Ile | Ala | Leu | Arg | Gly | Gly | |
| | | | | 290 | | | | | 295 | | | | | 300 | |
| Gly | Ala | Ala | Asp | Pro | Pro | Phe | Cys | Pro | His | Tyr | Glu | Lys | Val | Ser | |
| | | | | 305 | | | | | 310 | | | | | 315 | |

[illegible]

(2) INFORMATION FOR SEQ ID NO:3:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | |
|------------|------------|------------|------------|------------|------|
| CCCCCATTC | TGGGCCGGGG | GGCGTGCAG | TCGGGGCCCT | GCTGCTGCTG | 300 |
| GGGGTTTTGG | GGCTGGTGTC | TGGGCTCAGC | CTGGAGCCTG | TCTACTGGAA | 350 |
| CTCGGCGAAT | AAGAGGTTCC | AGGCAGAGGG | TGGTTATGTG | CTGTACCCTC | 400 |
| AGATCGGGGA | CCGGCTAGAC | CTGCTCTGCC | CCCGGGCCCC | GCCTCCTGGC | 450 |
| CCTCACTCCT | CTCCTAATTA | TGAGTTCTAC | AAGCTGTACC | TGGTAGGGGG | 500 |
| TGCTCAGGGC | CGGCGCTGTG | AGGCACCCCC | TGCCCCAAAC | CTCCTTCTCA | 550 |
| CTTGTGATCG | CCCAGACCTG | GATCTCCGCT | TCACCATCAA | GTTCCAGGAG | 600 |
| TATAGCCCTA | ATCTCTGGGG | CCACGAGTTC | CGCTCGCACC | ACGATTACTA | 650 |
| CATCATTGCC | ACATCGGATG | GGACCCGGGA | GGGCCTGGAG | AGCCTGCAGG | 700 |
| GAGGTGTGTG | CCTAACCAGA | GGCATGAAGG | TGCTTCTCCG | AGTGGGACAA | 750 |
| AGTCCCCGAG | GAGGGGCTGT | CCCCCGAAAA | CCTGTGTCTG | AAATGCCCAT | 800 |
| GGAAAGAGAC | CGAGGGGCAG | CCCACAGCCT | GGAGCCTGGG | AAGGAGAACC | 850 |
| TGCCAGGTGA | CCCCACCAGC | AATGCAACCT | CCCGGGGTGC | TGAAGGCCCC | 900 |
| CTGCCCCCTC | CCAGCATGCC | TGCAGTGGCT | GGGGCAGCAG | GGGGGCTGGC | 950 |
| GCTGCTCTTG | CTGGGCGTGG | CAGGGGCTGG | GGGTGCCATG | TGTTGGCGGA | 1000 |
| GACGGCGGGC | CAAGCCTTCG | GAGAGTCGCC | ACCCTGGTCC | TGGCTCCTTC | 1050 |
| GGGAGGGGAG | GGTCTCTGGG | CCTGGGGGGT | GGAGGTGGGA | TGGGACCTCG | 1100 |
| GGAGGCTGAG | CCTGGGGAGC | TAGGGATAGC | TCTGCGGGGT | GGCGGGGCTG | 1150 |
| CAGATCCCCC | CTTCTGCCCC | CACTATGAGA | AGGTGAGTGG | TGACTATGGG | 1200 |
| CATCCTGTGT | ATATCGTGCA | GGATGGGCCC | CCCCAGAGCC | CTCCAAACAT | 1250 |
| CTACTACAAG | GTATGAGGGC | TCCTCTCAGC | TGGCTATCCT | GAATCCAGCC | 1300 |
| CTTCTTGGGG | TGCTCCTCCA | GTTTAATTCC | TGGTTTGAGG | GACACCTCTA | 1350 |
| ACATCTCGGC | CCCCTGTGCC | CCCCCAGCCC | CTTCACTCCT | CCCGGCTGCT | 1400 |
| GTCCTCGTCT | CCACTTTTAG | GATTCCTTAG | GATTCCCCT | GCCCCACTTC | 1450 |
| CTGCCCTCCC | GTTTGGCCAT | GGGTGCCCCC | CTCTGTCTCA | GTGTCCCTGG | 1500 |

ATCCTTTTTC CTTGGGGAGG GGCACAGGCT CAGCCTCCTC TCTGACCATG 1550
 ACCCAGGCAT CCTTGTCCCC CTCACCCACC CAGAGCTAGG GGCGGGAACA 1600
 GCCCACCTTT TGGTTGGCAC CGCCTTCTTT CTGCCTCTCA CTGGTTTTCT 1650
 CTTCTCTATC TCTTATTCTT TCCCTCTCTT CCGTCTCTAG GTCTGTTCTT 1700
 CTTCCCTAGC ATCCTCCTCC CCACATCTCC TTTCACCCTC TTGGCTTCTT 1750
 ATCCTGTGCC TCTCCCATCT CCTGGGTGGG GGCATCAAAG CATTTCTCCC 1800
 CTTAGCTTTC AGCCCCCTT CTGACCTCTC ATACCAACCA CTCCCCTCAG 1850
 TCTGCCAAAA ATGGGGGCCT TATGGGGAAG GCTCTGACAC TCCACCCCAG 1900
 CTCAGGCCAT GGGCAGCAGG GCTCCATTCT CTGGCCTGGC CCAGGCCTCT 1950
 ACATACTTAC TCCAGCCATT TGGGGTGGTT GGGTCATGAC AGCTACCATG 2000
 AGAAGAAGTG TCCCGTTTTG TCCAGTGGCC AATAGCAAGA TATGAACCGG 2050
 TCGGGACATG TATGGACTTG GTCTGATGCT GAATGGGCCA CTTGGGACCG 2100
 GAAGTGACTT GCTCCAGACA AGAGGTGACC AGGCCCGGAC AGAAATGGCC 2150
 TGGGAAGTAG CAGAAGCAGT GCAGCAGGAA CTGGAAGTGC CTTCATCCAG 2200
 GACAGGAAGT AGCACTTCTG AAACAGGAAG TGGTCTGGCT GGAACTCCAA 2250
 GTGGCTTAGT CTGGGGGATC AGGAGGTGGG AGGTGGATGG TTCTTATTCT 2300
 GTGGAGAAGA AGGGCGGGAA GAACTTCCTT TCAGGAGGAA GCTGGAACCT 2350
 ACTGACTGTA AGAGGTTAGA GGTGGACCGA 2380

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Pro | Pro | His | Ser | Gly | Pro | Gly | Gly | Val | Arg | Val | Gly | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | |
| Leu | Leu | Leu | Leu | Gly | Val | Leu | Gly | Leu | Val | Ser | Gly | Leu | Ser | Leu |
| | | | | 20 | | | | 25 | | | | | 30 | |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGACAAAGTC CCGAGGAGGG GCTGTCCCCC GAAAACCTGT GTCTGAAATG 50
CCCATGGAAA 60

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGGTTCTCC TTCCCCAGGC TCCCAGGCTG TGGGCTGCCC CTCGGTCTCT 50
TTCCATGGGC 60

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Pro Gly Gln Arg Trp Leu Gly Lys Trp Leu Val Ala
1 5 10 15
Met Val Val Trp Ala Leu Cys Arg Leu Ala Thr Pro Leu Ala Lys
20 25 30

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Glu | Pro | Val | Ser | Trp | Ser | Ser | Leu | Asn | Pro | Lys | Phe | Leu | 35 | 40 | 45 |
| Ser | Gly | Lys | Gly | Leu | Val | Ile | Tyr | Pro | Lys | Ile | Gly | Asp | Lys | Leu | 50 | 55 | 60 |
| Asp | Ile | Ile | Cys | Pro | Arg | Ala | Glu | Ala | Gly | Arg | Pro | Tyr | Glu | Tyr | 65 | 70 | 75 |
| Tyr | Lys | Leu | Tyr | Leu | Val | Arg | Pro | Glu | Gln | Ala | Ala | Ala | Cys | Ser | 80 | 85 | 90 |
| Thr | Val | Leu | Asp | Pro | Asn | Val | Leu | Val | Thr | Cys | Asn | Arg | Pro | Glu | 95 | 100 | 105 |
| Gln | Glu | Ile | Arg | Phe | Thr | Ile | Lys | Phe | Gln | Glu | Phe | Ser | Pro | Asn | 110 | 115 | 120 |
| Tyr | Met | Gly | Leu | Glu | Phe | Lys | Lys | His | His | Asp | Tyr | Tyr | Ile | Thr | 125 | 130 | 135 |
| Ser | Thr | Ser | Asn | Gly | Ser | Leu | Glu | Gly | Leu | Glu | Asn | Arg | Glu | Gly | 140 | 145 | 150 |
| Gly | Val | Cys | Arg | Thr | Arg | Thr | Met | Lys | Ile | Ile | Met | Lys | Val | Gly | 155 | 160 | 165 |
| Gln | Asp | Pro | Asn | Ala | Val | Thr | Pro | Glu | Gln | Leu | Thr | Thr | Ser | Arg | 170 | 175 | 180 |
| Pro | Ser | Lys | Glu | Ala | Asp | Asn | Thr | Val | Lys | Met | Ala | Thr | Gln | Ala | 185 | 190 | 195 |
| Pro | Gly | Ser | Arg | Gly | Ser | Leu | Gly | Asp | Ser | Asp | Gly | Lys | His | Glu | 200 | 205 | 210 |
| Thr | Val | Asn | Gln | Glu | Glu | Lys | Ser | Gly | Pro | Gly | Ala | Ser | Gly | Gly | 215 | 220 | 225 |
| Ser | Ser | Gly | Asp | Pro | Asp | Gly | Phe | Phe | Asn | Ser | Lys | Val | Ala | Leu | 230 | 235 | 240 |
| Phe | Ala | Ala | Val | Gly | Ala | Gly | Cys | Val | Ile | Phe | Leu | Leu | Ile | Ile | 245 | 250 | 255 |
| Ile | Phe | Leu | Thr | Val | Leu | Leu | Leu | Lys | Leu | Arg | Lys | Arg | His | Arg | 260 | 265 | 270 |
| Lys | His | Thr | Gln | Gln | Arg | Ala | Ala | Ala | Leu | Ser | Leu | Ser | Thr | Leu | 275 | 280 | 285 |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Pro | Lys | Gly | Gly | Ser | Gly | Thr | Ala | Gly | Thr | Glu | Pro | Ser |
| | | | | 290 | | | | | 295 | | | | | 300 |
| Asp | Ile | Ile | Ile | Pro | Leu | Arg | Thr | Thr | Glu | Asn | Asn | Tyr | Cys | Pro |
| | | | | 305 | | | | | 310 | | | | | 315 |
| His | Tyr | Glu | Lys | Val | Ser | Gly | Asp | Tyr | Gly | His | Pro | Val | Tyr | Ile |
| | | | | 320 | | | | | 325 | | | | | 330 |
| Val | Gln | Glu | Met | Pro | Pro | Gln | Ser | Pro | Ala | Asn | Ile | Tyr | Tyr | Lys |
| | | | | 335 | | | | | 340 | | | | | 345 |
| Val | | | | | | | | | | | | | | |
| 346 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Arg | Arg | Asp | Ser | Val | Trp | Lys | Tyr | Cys | Trp | Gly | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Leu | Met | Val | Leu | Cys | Arg | Thr | Ala | Ile | Ser | Lys | Ser | Ile | Val | Leu |
| | | | | 20 | | | | | 25 | | | | | 30 |
| Glu | Pro | Ile | Tyr | Trp | Asn | Ser | Ser | Asn | Ser | Lys | Phe | Leu | Pro | Gly |
| | | | | 35 | | | | | 40 | | | | | 45 |
| Gln | Gly | Leu | Val | Leu | Tyr | Pro | Gln | Ile | Gly | Asp | Lys | Leu | Asp | Ile |
| | | | | 50 | | | | | 55 | | | | | 60 |
| Ile | Cys | Pro | Lys | Val | Asp | Ser | Lys | Thr | Val | Gly | Gln | Tyr | Glu | Tyr |
| | | | | 65 | | | | | 70 | | | | | 75 |
| Tyr | Lys | Val | Tyr | Met | Val | Asp | Lys | Asp | Gln | Ala | Asp | Arg | Cys | Thr |
| | | | | 80 | | | | | 85 | | | | | 90 |
| Ile | Lys | Lys | Glu | Asn | Thr | Pro | Leu | Leu | Asn | Cys | Ala | Lys | Pro | Asp |
| | | | | 95 | | | | | 100 | | | | | 105 |
| Gln | Asp | Ile | Lys | Phe | Thr | Ile | Lys | Phe | Gln | Glu | Phe | Ser | Pro | Asn |
| | | | | 110 | | | | | 115 | | | | | 120 |
| Leu | Trp | Gly | Leu | Glu | Phe | Gln | Lys | Asn | Lys | Asp | Tyr | Tyr | Ile | Ile |
| | | | | 125 | | | | | 130 | | | | | 135 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ser | Thr | Ser | Asn | Gly | Ser | Leu | Glu | Gly | Leu | Asp | Asn | Gln | Glu | Gly | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Gly | Val | Cys | Gln | Thr | Arg | Ala | Met | Lys | Ile | Leu | Met | Lys | Val | Gly | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Gln | Asp | Ala | Ser | Ser | Ala | Gly | Ser | Thr | Arg | Asn | Lys | Asp | Pro | Thr | |
| | | | | 170 | | | | | 175 | | | | | 180 | |
| Arg | Arg | Pro | Glu | Leu | Glu | Ala | Gly | Thr | Asn | Gly | Arg | Ser | Ser | Thr | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Thr | Ser | Pro | Phe | Val | Lys | Pro | Asn | Pro | Gly | Ser | Ser | Thr | Asp | Gly | |
| | | | | 200 | | | | | 205 | | | | | 210 | |
| Asn | Ser | Ala | Gly | His | Ser | Gly | Asn | Asn | Ile | Leu | Gly | Ser | Glu | Val | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Ala | Leu | Phe | Ala | Gly | Ile | Ala | Ser | Gly | Cys | Ile | Ile | Phe | Ile | Val | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Ile | Ile | Ile | Thr | Leu | Val | Val | Leu | Leu | Leu | Lys | Tyr | Arg | Arg | Arg | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| His | Arg | Lys | His | Ser | Pro | Gln | His | Thr | Thr | Thr | Leu | Ser | Leu | Ser | |
| | | | | 260 | | | | | 265 | | | | | 270 | |
| Thr | Leu | Ala | Thr | Pro | Lys | Arg | Ser | Gly | Asn | Asn | Asn | Gly | Ser | Glu | |
| | | | | 275 | | | | | 280 | | | | | 285 | |
| Pro | Ser | Asp | Ile | Ile | Ile | Pro | Leu | Arg | Thr | Ala | Asp | Ser | Val | Phe | |
| | | | | 290 | | | | | 295 | | | | | 300 | |
| Cys | Pro | His | Tyr | Glu | Lys | Val | Ser | Gly | Asp | Tyr | Gly | His | Pro | Val | |
| | | | | 305 | | | | | 310 | | | | | 315 | |
| Tyr | Ile | Val | Gln | Glu | Met | Pro | Pro | Gln | Ser | Pro | Ala | Asn | Ile | Tyr | |
| | | | | 320 | | | | | 325 | | | | | 330 | |
| Tyr | Lys | Val | | | | | | | | | | | | | |
| | | | | 333 | | | | | | | | | | | |